

Figure 1: 108P5H8 SSH sequence of 448 nucleotides (SEQ ID: 2568)

```
1 GATCCAGATT TCTCTGCACA CTGGACTTCG TAGAGTAAGT GTGGTAGACA AAGAGACTAC
61 ACTGCACAAC CACCAGTGAA TATCATTGCT AAGAAGACTT TGGGTCGTGT TTCTCAGCCA
121 CTCTCACAGC TTTTGTAGAC TTATTTGATT TTGAAACAAG CAGTTAGCTA AATCTATTTT
181 CCTTTTATGC ATATATGTTA ATTGGCTCAA CTTAATATGG TGTCTTACA GAATATGAGC
241 CCATTTGAAA TAAGGTTTTA GGCAATTTTG CTGTTGGCTC TGATTTGTAT ATAGCAAATT
301 TAAAGGTACA GAGTGTTCCT TAGATAGAAG ATTAGTTCAT TTGGTTCATT TTGTCTTTGA
361 AGCAAGCCAA GCTCATGAGC CAGTTGGTTA TTTGTCATAA ATGAACACCC ATCACTATAT
421 GCTATGTTGA GGGGAGGCAA GGCTGATC
```

Figure 2A. The cDNA (SEQ ID. NO. :2569) and amino acid sequence (SEQ ID. NO. :2570) of 108P5H8 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 253-1542 including the stop codon.

```
1 gccggcctccagcagcgggcgcggcgggcgcgagcacgacccactctcctgcggccgcg
61 ggtggagcagcgcgagccgcctcgctgagccggccggggcgaggatgagttgcggc
121 cccgcggcagcgcgccagcatggggaggagcgcgcggcactgccctcgagaactggcgct
181 ccggtgaagttaggcgcgcggccggtccgcctccccaagccgttcgcacccgcggccgcg
1 M A G S G A W K R L K S M L R K
241 tcagcctctgccATGCCGGCTCTGGCGCTGGAAGCGCCTCAAATCTATGCTAAGGAAG
17 D D A P L F L N D T S A F D F S D E A G
301 GATGATGCGCCGCTGTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGG
37 D E G L S R F N K L R V V V A D D G S E
361 GACGAGGGGCTTTCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAA
57 A P E R P V N G A H P T L Q A D D D S L
421 GCCCCGAAAGGCCTGTTAACGGGGCGCACCCGACCTCCAGGCCGACGATGATTCCTTA
77 L D Q D L P L T N S Q L S L K V D S C D
481 CTGGACCAAGACTTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGAC
97 N C S K Q R E I L K Q R K V K A R L T I
541 AACTGCAGCAAACAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATT
117 A A V L Y L L F M I G E L V G G Y I A N
601 GCTGCCGTTCTGTACTTGCTTTTCATGATTGGAGAAGTTGTAGGTGGATAACATTGCAAAT
137 S L A I M T D A L H M L T D L S A I I L
661 AGCCTAGCAATCATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTC
157 T L L A L W L S S K S P T K R F T F G F
721 ACCCTGCTTGCTTTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATT
177 H R L E V L S A M I S V L L V Y I L M G
781 CATCGCTTAGAGGTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGA
```

Figure 2A continued

197 F L L Y E A V Q R T I H M N Y E I N G D
841 TTCCTCTTATATGAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGAT
217 I M L I T A A V G V A V N V I M G F L L
901 ATAATGCTCATCACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTG
237 N Q S G H R H S H S H S L P S N S P T R
961 AACCACTCTGGTCACCGTCACTCCCATTCCTGCCTTCAAATTCCTTACCAGA
257 G S G C E R N H G Q D S L A V R A A F V
1021 GGTTCTGGGTGTGAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTGTGTA
277 H A L G D L V Q S V G V L I A A Y I I R
1081 CATGCTTTGGGAGATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGA
297 F K P E Y K I A D P I C T Y V F S L L V
1141 TTCAAGCCAGAATACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTG
317 A F T T F R I I W D T V V I I L E G V P
1201 GCTTTTACAACATTTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCA
337 S H L N V D Y I K E A L M K I E D V Y S
1261 AGCCATTTGAATGTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCA
357 V E D L N I W S L T S G K S T A I V H I
1321 GTCGAAGATTTAAATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATA
377 Q L I P G S S S K W E E V Q S K A N H L
1381 CAGCTAATTCCTGGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTA
397 L L N T F G M Y R C T I Q L Q S Y R Q E
1441 TTATTGAACACATTTGGCATGTATAGATGTACTATTGAGCTTCAGAGTTACAGGCAAGAA
417 V D R T C A N C Q S S S P *
1501 GTGGACAGAACTTGTGCAAATTGTGAGAGTTCTAGTCCCTAAAtttatgtattttgggaa
1561 ctctgccttatttctcctgcagtcacagacttgagagcaataaatgcaaacctaaatga
1621 gaaaatggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccc
1681 cagcctgacagtgctagtcctctgtttaatggtaaaaggagactttgccataattttcaga
1741 tgaagatgtttcccaaactgtttacagaatgagatgtgactctacagatacctcatag
1801 aagacaatccaagatcatacttcattaacttgacagagtacgtgtcttaaggaagcatc
1861 aagaattcaatatatttgcatTTAAAAatactttttaaggccattttatattaagccagtg
1921 tggaaaactgaattttttttattatgtataataatctcgacacccagcttctggaattgc
1981 tgctttctttttacagaaattactacccaacagatttcaggaagtactagtagttatccc
2041 aaaagtggaaataagcatgtattcctaagtgttcagaaatgttttatttcacacataagt
2101 cttaatgttattgttatgattatactttataaacaaccttttccagatgctacagggttt
2161 tgaatctcaaagttaacatttttcattatttgaatcttagaaccaaatctttatttatt
2221 gtggtcactgttattaaatgatttaggaaatactttcaatattattctgaatggctgaag
2281 ttagtcttaaaactcaaattactatatgatgatttaaaacaaaataaaagagcgaggatgg
2341 ggaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :2571) and amino acid sequence (SEQ ID. NO. :2572) of 108P5H8 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```
1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F D F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTCCGAAGCCCCGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAAGTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAATCACCAACCAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTGTGAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCACTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCTCCCTGCCTTCAAATTCCTTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGATCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
961 TTTCAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L
```

Figure 2B continued

1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttggggactcctgccttat
1321 ttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaaatggaatc
1381 cctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagcctgacagt
1441 gctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaagatgtttc
1501 ccaaactgtttacagaatgagatgtgactctacagatacctcatag

Figure 2C. The cDNA (SEQ ID. NO. :2573) and amino acid sequence (SEQ ID. NO. :2574) of 108P5H8 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```
1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F E F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGAGTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGGAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCCCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAATCACCAACCAAAGATTACCTTTGGATTTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAAGTATCCATATGAAGTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCCTCAAATCCCCTACCAGAGGTTCTGGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATCTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGACCCCATCTGTACATACGATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
961 TTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTGAAT
```

Figure 2C continued

341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAttttatgtattgttttagcattgctgaatt
1321 cactttattttatcctgcagtcacagacttgagagcaataaatgcaaactaatgagaaa
1381 atggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagc
1441 ctgacagtgctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaa
1501 gatgtttcccaaactgtttacagaatgagatgtgactcctacagatacctcatag

Figure 4:

Figure 4A Nucleic acid sequence alignment of the 3 variants of 108P5H8. (SEQ ID NOS: 2569, 2571 & 2573). Highlighted in yellow and underlined are the variations between the variants. The ORF extends from nucleotides 253-1542 of 108P5H8 v.1.

1	15	16	30	31	45	46	60	61	75	76	90
v.1	GGCGGCTCCAGCAG	CGGGCGCGGGGGCGG	CGAGACGACCCCGC	TCTCCTGCGGCGCGG	GGTGGAGCAGCGCGA	GGCGGCTCGCTGAG					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
91	105	106	120	121	135	136	150	151	165	166	180
v.1	CGGCGCGGGGCGGG	GAGATCAGTTGCGG	CCCGCGGACGCGCC	CAGGATGGGAGGGA	CGCGGCGCACTGCC	TCGAGAACTGGCGCT					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
181	195	196	210	211	225	226	240	241	255	256	270
v.1	CCGGTGAAGTAGGCG	CGCGCGCGCGTCCGC	CTCCCCAAGCCGTT	CCGCACCGCGCGCGC	TCAGCCTCTGCCATG	GCCGGCTCTGGCGCG					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
271	285	286	300	301	315	316	330	331	345	346	360
v.1	TGAAGCGCCTCAA	TCTATGCTAAGGAAG	GATGATGCGCGCGTG	TTTTTAAATGACACC	AGCGCCTTTGAGTTC	TCGGATGAGGCGGGG					
v.2	TGAAGCGCCTCAA	TCTATGCTAAGGAAG	GATGATGCGCGCGTG	TTTTTAAATGACACC	AGCGCCTTTGAGTTC	TCGGATGAGGCGGGG					
v.3	TGAAGCGCCTCAA	TCTATGCTAAGGAAG	GATGATGCGCGCGTG	TTTTTAAATGACACC	AGCGCCTTTGAGTTC	TCGGATGAGGCGGGG					
361	375	376	390	391	405	406	420	421	435	436	450
v.1	GACGAGGGGCTTTCT	CGGTTCAACAACTT	CGAGTTGTGTGGCC	GATGACGGTTCCGAA	GCCCGGAAAGGCCT	GTTAACGGGCGGCAC					
v.2	GACGAGGGGCTTTCT	CGGTTCAACAACTT	CGAGTTGTGTGGCC	GATGACGGTTCCGAA	GCCCGGAAAGGCCT	GTTAACGGGCGGCAC					
v.3	GACGAGGGGCTTTCT	CGGTTCAACAACTT	CGAGTTGTGTGGCC	GATGACGGTTCCGAA	GCCCGGAAAGGCCT	GTTAACGGGCGGCAC					
451	465	466	480	481	495	496	510	511	525	526	540
v.1	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCCAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCTCTGTGAC					
v.2	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCCAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCTCTGTGAC					
v.3	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCCAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCTCTGTGAC					

Figure 4 continued

541	555	556	570	571	585	586	600	601	615	616	630
v.1	AACTGCAGCAAAACAG	AGAGAGATACCTGAAG	CAGAGAAAGGTGAAA	GCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTCATGATT					
v.2	AACTGCAGCAAAACAG	AGAGAGATACCTGAAG	CAGAGAAAGGTGAAA	GCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTCATGATT					
v.3	AACTGCAGCAAAACAG	AGAGAGATACCTGAAG	CAGAGAAAGGTGAAA	GCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTCATGATT					
631	645	646	660	661	675	676	690	691	705	706	720
v.1	GGAGAACTTGTAGGT	GGATACATTGCAAT	AGCCTAGCAATCATG	ACAGATGCACTTCAT	ATGTTAACTGACCTA	AGCGCCATCATATCTC					
v.2	GGAGAACTTGTAGGT	GGATACATTGCAAT	AGCCTAGCAATCATG	ACAGATGCACTTCAT	ATGTTAACTGACCTA	AGCGCCATCATATCTC					
v.3	GGAGAACTTGTAGGT	GGATACATTGCAAT	AGCCTAGCAATCATG	ACAGATGCACTTCAT	ATGTTAACTGACCTA	AGCGCCATCATATCTC					
721	735	736	750	751	765	766	780	781	795	796	810
v.1	ACCCTGCTTGCCTTG	TGGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACCTTTGGATT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT					
v.2	ACCCTGCTTGCCTTG	TGGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACCTTTGGATT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT					
v.3	ACCCTGCTTGCCTTG	TGGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACCTTTGGATT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT					
811	825	826	840	841	855	856	870	871	885	886	900
v.1	AGTGTGCTGTGGTG	TATATACTTATGGGA	TTCCTCTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACTAT	GAATAAATGGAGAT					
v.2	AGTGTGCTGTGGTG	TATATACTTATGGGA	TTCCTCTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACTAT	GAATAAATGGAGAT					
v.3	AGTGTGCTGTGGTG	TATATACTTATGGGA	TTCCTCTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACTAT	GAATAAATGGAGAT					
901	915	916	930	931	945	946	960	961	975	976	990
v.1	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAATGTAATA	ATGGGGTTTCTGTTG	AACCAAGTCTGGTCAC	CGTCACTCCCATTC					
v.2	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAATGTAATA	ATGGGGTTTCTGTTG	AACCAAGTCTGGTCAC	CGTCACTCCCATTC					
v.3	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAATGTAATA	ATGGGGTTTCTGTTG	AACCAAGTCTGGTCAC	CGTCACTCCCATTC					
991	1005	1006	1020	1021	1035	1036	1050	1051	1065	1066	1080
v.1	CACCTCCCTGCCCTTCA	AATCCCCCTACCCAGA	GGTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTGTA					
v.2	CACCTCCCTGCCCTTCA	AATCCCCCTACCCAGA	GGTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTGTA					
v.3	CACCTCCCTGCCCTTCA	AATCCCCCTACCCAGA	GGTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTGTA					
1081	1095	1096	1110	1111	1125	1126	1140	1141	1155	1156	1170
v.1	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGATAAC	AAGATTGCTGAGCCCC					
v.2	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGATAAC	AAGATTGCTGAGCCCC					
v.3	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGATAAC	AAGATTGCTGAGCCCC					
1171	1185	1186	1200	1201	1215	1216	1230	1231	1245	1246	1260

Figure 4 continued

v. 1	ATCTGTACATACGTA	TTTTTCATTACTTGTG	GCTTTTACAACATTT	CGAATCATATGGGAT	ACAGTAGTTATAATA	CTAGAAGGTGTGCCA					
v. 2	ATCTGTACATACGTA	TTTTTCATTACTTGTG	GCTTTTACAACATTT	CGAATCATATGGGAT	ACAGTAGTTATAATA	CTAGAAGGTGTGCCA					
v. 3	ATCTGTACATACGTA	TTTTTCATTACTTGTG	GCTTTTACAACATTT	CGAATCATATGGGAT	ACAGTAGTTATAATA	CTAGAAGGTGTGCCA					
1261	1275	1276	1290	1291	1305	1306	1320	1321	1335	1336	1350
v. 1	AGCCATTTGAATGPA	GACTATATCAAGAA	GCTTTGATGAAATA	GAAGATGTATATTCA	GTCGAAGATTAAAT	ATCTGGTCTCTCACT					
v. 2	AGCCATTTGAATGPA	GACTATATCAAGAA	GCTTTGATGAAATA	GAAGATGTATATTCA	GTCGAAGATTAAAT	ATCTGGTCTCTCACT					
v. 3	AGCCATTTGAATGPA	GACTATATCAAGAA	GCTTTGATGAAATA	GAAGATGTATATTCA	GTCGAAGATTAAAT	ATCTGGTCTCTCACT					
1351	1365	1366	1380	1381	1395	1396	1410	1411	1425	1426	1440
v. 1	TCAGGAAAATCTACT	GCCATAGTTCACATA	CAGCTAATTCCTGGA	AGTTTCATCTAAATGG	GAGGAAGTACAGTCC	AAAGCAAACCATTTA					
v. 2	TCAGGAAAATCTACT	GCCATAGTTCACATA	CAGCTAATTCCTGGA	AGTTTCATCTAAATGG	GAGGAAGTACAGTCC	AAAGCAAACCATTTA					
v. 3	TCAGGAAAATCTACT	GCCATAGTTCACATA	CAGCTAATTCCTGGA	AGTTTCATCTAAATGG	GAGGAAGTACAGTCC	AAAGCAAACCATTTA					
1441	1455	1456	1470	1471	1485	1486	1500	1501	1515	1516	1530
v. 1	TTATTTGAACACATTT	GGCATGTATAGATGT	ACTATTTCAGCTTCAG	AGTTACAGGCAAGAA	GTTGACAGAACTTGT	GCAATTTGTTCAGAGT					
v. 2	TTATTTGAACACATTT	GGCATGTATAGATGT	ACTATTTCAGCTTCAG	AGTTACAGGCAAGAA	GTTGACAGAACTTGT	GCAATTTGTTCAGAGT					
v. 3	TTATTTGAACACATTT	GGCATGTATAGATGT	ACTATTTCAGCTTCAG	AGTTACAGGCAAGAA	GTTGACAGAACTTGT	GCAATTTGTTCAGAGT					
1531	1545	1546	1560	1561	1575	1576	1590	1591	1605	1606	1620
v. 1	TCAGTCCCTAAATTT	TATGTATTT---TTGGG	AACTCTCTG---TTTC	CTTATTTATCTCTGCA	GTCACAGACTTGAGA	GCAATTAATGCAAAAC					
v. 2	TCAGTCCCTAAATTT	TATGTATTT---TTGGG	AACTCTCTG---TTTC	CTTATTTATCTCTGCA	GTCACAGACTTGAGA	GCAATTAATGCAAAAC					
v. 3	TCAGTCCCTAAATTT	TATGTATTT---TTGGG	AACTCTCTG---TTTC	CTTATTTATCTCTGCA	GTCACAGACTTGAGA	GCAATTAATGCAAAAC					
1621	1635	1636	1650	1651	1665	1666	1680	1681	1695	1696	1710
v. 1	CTAAATGAGAAAAATG	GAATCCCTGACAGCT	GTGTCCGTATCAAGC	ATCAGTCTCTCAAAC	AGTTGCCCGAGCTG	ACAGTGGTAGTCTCT					
v. 2	CTAAATGAGAAAAATG	GAATCCCTGACAGCT	GTGTCCGTATCAAGC	ATCAGTCTCTCAAAC	AGTTGCCCGAGCTG	ACAGTGGTAGTCTCT					
v. 3	CTAAATGAGAAAAATG	GAATCCCTGACAGCT	GTGTCCGTATCAAGC	ATCAGTCTCTCAAAC	AGTTGCCCGAGCTG	ACAGTGGTAGTCTCT					
1711	1725	1726	1740	1741	1755	1756	1770	1771	1785	1786	1800
v. 1	GTTTAAATGGTAAAG	GAGACTTTGGCATAA	TTTTCAGATGAAGAT	GTTTCCCAAAACACTG	TTTACAGAATGAGAT	GTGACTC-TACAGAT					
v. 2	GTTTAAATGGTAAAG	GAGACTTTGGCATAA	TTTTCAGATGAAGAT	GTTTCCCAAAACACTG	TTTACAGAATGAGAT	GTGACTC-TACAGAT					
v. 3	GTTTAAATGGTAAAG	GAGACTTTGGCATAA	TTTTCAGATGAAGAT	GTTTCCCAAAACACTG	TTTACAGAATGAGAT	GTGACTC-TACAGAT					
1801	1815	1816	1830	1831	1845	1846	1860	1861	1875	1876	1890

Figure 4 continued

v.1	ACCTCATAGAAGACA	ATCCAAGATCATACT	TCATTAACCTTGACAG	AGTACGTGTCTTAAA	GGAAGCATCAAGAAT	TCAATATTTGCATTT
v.2	ACCTCATAG-----	-----	-----	-----	-----	-----
v.3	ACCTCATAG-----	-----	-----	-----	-----	-----
1891	1905 1906	1920 1921	1935 1936	1950 1951	1965 1966	1980
v.1	AAAAATACTTTTTAA	GGCCATTTTATATTA	AGCCAGTGTGGAAA	ACTGAATTTTTTTTA	TTATGTATATAATC	TCGACACCCAGCTTC
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
1981	1995 1996	2010 2011	2025 2026	2040 2041	2055 2056	2070
v.1	TGGAATTGCTGCTTT	CTTTTACAGAAAT	ACTACCCACAGATT	TCAGGAAGTACTAGT	AGTTATCCCAAAGT	GGATAAGCATGTAT
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2071	2085 2086	2100 2101	2115 2116	2130 2131	2145 2146	2160
v.1	TCCTAAGTGTTCAG	AAATGTTTATTTCA	CACATAAGTCTTAAT	GTTATTGTTATGATT	ATACTTTATAAACAA	OCCTTTCCAGATGCT
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2161	2175 2176	2190 2191	2205 2206	2220 2221	2235 2236	2250
v.1	ACAGGGTTTTGAATC	TCAAAGTTTACATTT	TTCAATTATTGTAAT	CTTAGAACCAAAATCT	TTATTTATTGTGGTC	ACTGTTATTAAATGA
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2251	2265 2266	2280 2281	2295 2296	2310 2311	2325 2326	2340
v.1	TTTAGGAAATACTTT	CAATATTATCTGAA	TGGCTGAAGTTAGTC	TTAAACTCAAATTAC	TATATGATGATTAA	AACAAAATAAAGAG
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2341	2355 2356	2370	2364	1548	1557	
v.1	CGAGGATGGGAAAA	AAAAAAAAAAAAAA	AAA	---	---	
v.2	-----	-----	---	---	---	
v.3	-----	-----	---	---	---	